

L Number	Hits	Search Text	DB	Time stamp
1	6	vogeli-gabriel.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:29
2	20	lind-peter.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:29
3	12	parodi-luis-a.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:30
4	3	wood-linda-s.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:30
5	2	hiebsch-ronald-r.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:30
6	3085	g adj protein adj coupled adj receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:31
7	1174	(g adj protein adj coupled adj receptor) same human	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:32

09714449 Results

SEQ ID NO: 85

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
c	1	1020	100.0	1020	6	AX147840	AX147840 Sequence
	2	980.8	96.2	1081	6	AX458238	AX458238 Sequence
	3	980.8	96.2	1092	9	AF370886	AF370886 Homo sapi
	4	980.8	96.2	1414	9	AB065877	AB065877 Homo sapi
	5	980.8	96.2	9905	6	AX379470	AX379470 Sequence
	6	980.8	96.2	67645	9	AL356486	AL356486 Human DNA
	7	980.8	96.2	156555	9	AC026756	AC026756 Homo sapi
	8	979.2	96.0	1729	6	AX191332	AX191332 Sequence
	9	977.8	95.9	1014	6	AX148186	AX148186 Sequence
	10	977.8	95.9	1014	6	AX379468	AX379468 Sequence
	11	977.8	95.9	1014	6	AX384211	AX384211 Sequence
	12	977.8	95.9	1014	9	AB083598	AB083598 Homo sapi
	13	977.8	95.9	1014	9	AF411109	AF411109 Homo sapi
	14	976.2	95.7	1014	6	AX305130	AX305130 Sequence
	15	976.2	95.7	1014	6	AX464561	AX464561 Sequence
	16	701.4	68.8	202838	2	AC108794	AC108794 Mus muscu
c	17	578	56.7	578	6	AX147814	AX147814 Sequence
	18	335	32.8	2245	6	AX384210	AX384210 Sequence

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	1020	100.0	1020	22	AAH51011	Human nGPCR54 codi	
2	980.8	96.2	1288	24	ABL56197	Human P2Y1-li enco	
3	980.8	96.2	5435	24	ABL56198	Human P2Y1-li enco	
4	980.8	96.2	9905	24	AAK98324	Human purinergic-r	
5	979.2	96.0	1729	22	AAS08362	Human cDNA encodin	
6	979.2	96.0	1729	23	ABV24026	Human prostate exp	
7	979.2	96.0	1729	23	ABV25767	Human prostate exp	
8	979.2	96.0	1729	23	ABV29909	Human prostate exp	
9	979.2	96.0	1729	23	ABV30024	Human prostate exp	
10	977.8	95.9	1014	22	AAS07948	Human cDNA encodin	
11	977.8	95.9	1014	24	ABN85630	Human P2Y-like rec	
12	977.8	95.9	1014	24	ABK11381	Human DNA encoding	
13	977.8	95.9	1014	24	AAK98323	Human purinergic-r	
14	976.2	95.7	1014	24	ABQ78847	Human G-protein co	
15	976.2	95.7	1014	24	AAD34278	Human AXOR89 (G-pr	
16	976.2	95.7	1014	24	AAD26370	Human G-protein co	
17	974.8	95.6	1011	24	AAL43942	Human G protein-co	
18	794.8	77.9	831	24	ABN85629	Human P2Y-like rec	
19	726.2	71.2	1313	22	AAK52430	Human polynucleoti	
c	20	578	56.7	578	22	AAH50998	Human nGPCR54 codi
c	21	562.8	55.2	740	23	ABV15662	Human prostate exp
c	22	476.6	46.7	545	22	ABA08326	Human P2Y purinoce
c	23	476.6	46.7	545	22	AAK53414	Human polynucleoti
c	24	426.2	41.8	539	23	ABV39127	Human prostate exp

RESULT 1

AAH51011

ID AAH51011 standard; DNA; 1020 BP.

XX

AC AAH51011;

XX

DT 28-AUG-2001 (first entry)

XX

DE Human nGPCR54 coding sequence #2.

XX

KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;

KW signal transduction; schizophrenia; thyroid disorder; renal failure;
KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KW cardiovascular disease; proliferative disorder; hormonal disorder;
KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KW attention deficit-hyperactivity disorder/attention deficit disorder;
KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KW neuroprotective; ds.
XX
OS Homo sapiens.
XX
PN WO200136473-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US31581.
XX
PR 16-NOV-1999; 99US-0165838.
PR 17-NOV-1999; 99US-0166071.
PR 19-NOV-1999; 99US-0166678.
PR 28-DEC-1999; 99US-0173396.
PR 22-FEB-2000; 2000US-0184129.
PR 28-FEB-2000; 2000US-0185421.
PR 28-FEB-2000; 2000US-0185554.
PR 02-MAR-2000; 2000US-0186530.
PR 03-MAR-2000; 2000US-0186811.
PR 09-MAR-2000; 2000US-0188114.
PR 17-MAR-2000; 2000US-0190310.
PR 21-MAR-2000; 2000US-0190800.
PR 20-APR-2000; 2000US-0198568.
PR 02-MAY-2000; 2000US-0201190.
PR 08-MAY-2000; 2000US-0203111.
PR 25-MAY-2000; 2000US-0207094.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
XX
DR WPI; 2001-389826/41.
DR P-PSDB; AAG80971.
XX
PT New G protein-coupled receptor (nGPCR-x) and its encoding
PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -
XX
PS Claim 4; Page 91; 261pp; English.
XX
CC The present invention relates to novel G protein-coupled receptors
CC (nGPCR_x; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present
CC sequence is the coding sequence for one such G protein-coupled receptor.
CC GPCRs are also known as seven transmembrane receptors and function in
CC signal transduction. The nGPCR_x coding sequences are useful for
CC screening a human to diagnose a disorder affecting the brain or a genetic
CC predisposition, specifically schizophrenia. nGPCR_x are useful for
CC identifying compounds useful for treating schizophrenia. Detection of
CC nGPCR_x in a sample is useful as a diagnostic tool for diseases or
CC disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,
CC CNS disorders, infections such as HIV-1, metabolic and cardiovascular
CC diseases, proliferative disorders and hormonal disorders. Modulators of
CC nGPCR_x activity have the utility for treating neurological disorders,
CC including schizophrenia, ADHD/ADD (attention deficit-hyperactivity
CC disorder/attention deficit disorder), and neuronal disorders such as
CC Alzheimer's disease, Parkinson's disease, migraine and senile dementia.
CC Additional disorders include inflammatory conditions (e.g. Crohn's
CC disease), rheumatoid arthritis, autoimmune disorders, cancers,
CC respiratory ailments such as asthma, and inflammatory diseases e.g.
CC inflammatory bowel disease.
XX
SQ Sequence 1020 BP; 261 A; 263 C; 190 G; 306 T; 0 other;

Query Match 100.0%; Score 1020; DB 22; Length 1020;
 Best Local Similarity 100.0%; Pred. No. 3.3e-287;
 Matches 1020; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 ACCATGAATGAGCCACTAGACTATTAGCAAATGCTTCTGATTCCCCGATTATGCAGCT	60
Db	1 ACCATGAATGAGCCACTAGACTATTAGCAAATGCTTCTGATTCCCCGATTATGCAGCT	60
Qy	61 GCTTTTGGAAATTGCACTGATGAAAACATCCCCTCAAGATGCACTACCTCCCTGTTATT	120
Db	61 GCTTTTGGAAATTGCACTGATGAAAACATCCCCTCAAGATGCACTACCTCCCTGTTATT	120
Qy	121 TATGGCATTATCTTCCTCGTGGGATTTCAGGCAATGCAGTAGTGTATCCACTTACATT	180
Db	121 TATGGCATTATCTTCCTCGTGGGATTTCAGGCAATGCAGTAGTGTATCCACTTACATT	180
Qy	181 TTCAAAATGAGACCTTGGAAAGAGCAGCACCATCATTATGCTGAACCTGGCTGCACAGAT	240
Db	181 TTCAAAATGAGACCTTGGAAAGAGCAGCACCATCATTATGCTGAACCTGGCTGCACAGAT	240
Qy	241 CTGCTGTATCTGACCAGCCTCCCCCTCCTGATTCACTACTATGCCAGTGGCGAAACTGG	300
Db	241 CTGCTGTATCTGACCAGCCTCCCCCTCCTGATTCACTACTATGCCAGTGGCGAAACTGG	300
Qy	301 ATCTTTGGAGATTCATGTGTAAGTTATCCGCTTCAGCTTCATTCAACCTGTATAGC	360
Db	301 ATCTTTGGAGATTCATGTGTAAGTTATCCGCTTCAGCTTCATTCAACCTGTATAGC	360
Qy	361 AGCATCCCTTCCACCTGTGTTCAGCATCTCCGCTACTGTGTGATCATTACCCAATG	420
Db	361 AGCATCCCTTCCACCTGTGTTCAGCATCTCCGCTACTGTGTGATCATTACCCAATG	420
Qy	421 AGCTGCTTTCCATTCAACAAACTCGATGTGCAAGTTGCTGTGCTGTGGTGATGTC	480
Db	421 AGCTGCTTTCCATTCAACAAACTCGATGTGCAAGTTGCTGTGCTGTGGTGATGTC	480
Qy	481 ATTTCACTGGTAGCTGCATTCCGATGACCTTCTGATCACATCAACCAACAGGACCAAC	540
Db	481 ATTTCACTGGTAGCTGCATTCCGATGACCTTCTGATCACATCAACCAACAGGACCAAC	540
Qy	541 AGATCAGCCTGTCTCGACCTCACCAAGTTGGATGAACACTCAATACTATTAAGTGGTACAAC	600
Db	541 AGATCAGCCTGTCTCGACCTCACCAAGTTGGATGAACACTCAATACTATTAAGTGGTACAAC	600
Qy	601 CTGATTGACTGCAAGTACTTCTGCCTCCCCCTGGTGTAGTGACACTTGCTATACC	660
Db	601 CTGATTGACTGCAAGTACTTCTGCCTCCCCCTGGTGTAGTGACACTTGCTATACC	660
Qy	661 ACGATTATCCACACTTGACCCATGGACTGCAAACACTGACAGCTGCCATTAGCAGAAAGCA	720
Db	661 ACGATTATCCACACTTGACCCATGGACTGCAAACACTGACAGCTGCCATTAGCAGAAAGCA	720
Qy	721 CGAAGGCTAACCAATTGCTACTCCTGCATTACGTATGTTTACCCCTCCATATC	780
Db	721 CGAAGGCTAACCAATTGCTACTCCTGCATTACGTATGTTTACCCCTCCATATC	780
Qy	781 TTGAGGGTCATTCAAGGATCGAACATCTCAGCCTGCTTCAATCAGTTGTTCCATTGAGAATC	840
Db	781 TTGAGGGTCATTCAAGGATCGAACATCTCAGCCTGCTTCAATCAGTTGTTCCATTGAGAATC	840
Qy	841 AGATCCATGAAGCTTACATCGTTCTAGACCATATTGCTGCTCTGAACACCTTGGTAAC	900
Db	841 AGATCCATGAAGCTTACATCGTTCTAGACCATATTGCTGCTCTGAACACCTTGGTAAC	900
Qy	901 CTGTTACTATATGTTGGTCAGCGACAACCTTCAGCAGGCTGTGCTCAACAGTGAGA	960
Db	901 CTGTTACTATATGTTGGTCAGCGACAACCTTCAGCAGGCTGTGCTCAACAGTGAGA	960
Qy	961 TGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACACCCTTGA	1020
Db	961 TGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACACCCTTGA	1020

No.	Score	Match	Length	DB	ID	Description
1	210	20.6	744	14	BM723768	BM723768 UI-E-EO1-
2	126.6	12.4	623	14	BQ038875	BQ038875 pgnlc.pk0
3	115.6	11.3	641	14	BQ396255	BQ396255 NISC_ng19
4	114.6	11.2	638	9	AL675845	AL675845 AL675845
5	109.4	10.7	877	12	BG402029	BG402029 602466748
6	108.8	10.7	663	13	BM426517	BM426517 pgf2n.pk0
c 7	107.4	10.5	1101	17	CNS0532S	AL318925 Tetradon
8	106.2	10.4	491	12	BG712193	BG712193 pglin.pk0
9	103	10.1	609	9	AL588350	AL588350 AL588350
10	102	10.0	520	9	AI663305	AI663305 uk27c10.y
11	100.4	9.8	2542	11	AK017378	AK017378 Mus muscu
12	100.4	9.8	3001	11	AK005013	AK005013 Mus muscu
13	100	9.8	422	10	BB847918	BB847918 BB847918
14	99.6	9.8	801	13	BG924078	BG924078 602823635
15	98.4	9.6	606	17	AZ953874	AZ953874 2M0219L17
16	97.2	9.5	851	13	BI833118	BI833118 603090834
c 17	95.8	9.4	408	13	BI401676	BI401676 MI-P-CP0-

RESULT 1

BM723768

LOCUS BM723768 744 bp mRNA linear EST 01-MAR-2002

DEFINITION UI-E-EO1-aix-g-16-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-aix-g-16-0-UI 5', mRNA sequence.

ACCESSION BM723768

VERSION BM723768.1 GI:19045099

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 744)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

source 1..744
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-EO1-aix-g-16-0-UI"
/clone_lib="UI-E-EO1"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was

constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 217 a 168 c 126 g 233 t
ORIGIN

Query Match 20.6%; Score 210; DB 14; Length 744;
Best Local Similarity 98.8%; Pred. No. 1.8e-51;
Matches 243; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

 Qy 775 CATATCTGAGGGTCATTCAAGGATCGAATCTCAGCCTGCTTCATACTAGTTGTTCCATTG 834
 |||||||
 Db 1 CATATCTGAGGGTCATT-C-GGATCGAATCTC-GCCTGCTTCATACTAGTTGTTCCATTG 58

 Qy 835 AGAACATCAGATCCATGAAGCTTACATCGTTCTAGACCATTATGCTGCTGAACACCTTT 894
 |||||||
 Db 59 AGAACATCAGATCCATGAAGCTTACATCGTTCTAGACCATT-A-GCTGCTCTGAACACCTTT 117

 Qy 895 GGTAACCTGTTACTATATGTGGTGGTCAGCGACAACCTTCAGCAGGCTGTGCTCAACA 954
 |||||||
 Db 118 GGTAACCTGTTACTATATGTGGTGGTCAGCGACAACCTTCAGCAGGCTGTGCTCAACA 177

 Qy 955 GTGAGATGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAAAC 1014
 |||||||
 Db 178 GTGAGATGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAAAC 237

 Qy 1015 CCTTGA 1020
 |||||
 Db 238 CCTTGA 243

AI663305

LOCUS AI663305 520 bp mRNA linear EST 10-MAY-1999
 DEFINITION uk27c10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
 IMAGE:1970226 5' similar to SW:P2YR_RAT P49651 P2Y PURINOCEPTOR 1
 ;, mRNA sequence.
 ACCESSION AI663305
 VERSION AI663305.1 GI:4766888
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 520)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,
 B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,
 E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Other_ESTs: uk27c10.x1
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:986966
Seq primer: custom primer used
High quality sequence stop: 490.
FEATURES Location/Qualifiers
source 1. .520
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1970226"
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
BASE COUNT 127 a 126 c 107 g 160 t
ORIGIN

```

Query Match      10.0%; Score 102; DB 9; Length 520;
Best Local Similarity 53.4%; Pred. No. 3.3e-19;
Matches 238; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

Qy   62 CTTTTGAAATTGCACTGATGAAAAACATCCACTCAAGATGCACTACCTCCCTGTTATT 121
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   73 CTTGTGAGAATTGGTTGGCAACAGAGGCTATCTGAATAAGTACTACCTCTGCATT 132
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   122 ATGGCATTATCTTCCTCGTGGGATTCCAGGCAATGCAGTAGTGATATCCACTTACATT 181
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   133 ATGCAATCGAGTTCATTTGGACTGCTGGGAATGTCAGTGTTGGCTACCTCT 192
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   182 TCAAAATGAGACCTTGGAAAGAGCAGCACCATTATGCTGAACCTGGCCTGCACAGATC 241
     ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   193 TCTGCATGAAGAACGGAACAGCAGCAATGTCTATCTTTAACCTTCCATCTGACT 252
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   242 TGCTGTATCTGACCAGCCTCCCCCTCCTGATTCACTACTATGCCAGTGGCGAAACTGGA 301
     ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   253 TTGCTTCTGTGCACCCCTCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 309
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   302 TCTTTGGAGATTCATGTGTAAGTTATCCGCTTCAGCTTCAACCTGTATAGCA 361
     ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   310 CCTATGGAGATGTTCTGTATAAGCAACCGATATGTGCTCACACCAACCTCTACACCA 369
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   362 GCATCCTCTCCTCACCTGTTCAAGCATCTCCGCTACTGTGTGATCATTACCCAATGA 421
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   370 GCATGCTTGTCACTGTCATTATCATGGACCGATATCTGCTCATGAAGTACCCGTCC 429
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   422 GCTGCTTCCATTCAACAAACTCGATGTGCAGTTGAGCCTGTGCTGTGGTGGATCA 481
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   430 GAGAACACTTCTACAAAAGAAGGAATTGCCATTAACTCGCTGGCTGTCTGGGCCT 489
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   482 TTTCACTGGTAGCTGTCATTCCGATG 507
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   490 TAGTGACCTTAGAAGTTCTACCCATG 515
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1768	100.0	336	22	AAG80971	Human nGPCR54 #2.
2	1603.5	90.7	337	22	AAU04584	Human G-protein co
3	1602.5	90.6	337	22	AAU04375	Human G-protein co
4	1602.5	90.6	337	23	AAO15399	Human G protein-co
5	1602.5	90.6	337	23	ABB81902	Human G-protein co
6	1602.5	90.6	337	23	ABB83819	Human P2Y-like rec
7	1602.5	90.6	337	23	AAE21803	Human AXOR89 (G-pr
8	1602.5	90.6	337	23	ABB79438	Human P2Y1-li. Ho
9	1602.5	90.6	337	23	AAU77600	Human P2Y1-like G
10	1602.5	90.6	337	23	AAO14027	Human purinergic-r
11	1602.5	90.6	337	23	AAE16171	Human G-protein co
12	1275.5	72.1	276	23	ABB83818	Human P2Y-like rec
13	1098	62.1	230	22	AAM79297	Human protein SEQ
14	997	56.4	192	22	AAG80958	Human nGPCR54 #1.
15	881.5	49.9	179	22	ABB11082	Human P2Y purinoce
16	881.5	49.9	179	22	AAM80281	Human protein SEQ
17	525.5	29.7	373	22	AAE04389	Human P2-purinergi
18	525.5	29.7	373	23	AAU10983	Purinergic recepto
19	525.5	29.7	373	23	AAU10984	Purinergic re

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	525.5	29.7	373	2	JC4737	G protein-coupled
2	525	29.7	362	2	S33733	G protein-coupled
3	523.5	29.6	373	2	JC4162	P2Y receptor - bov
4	444.5	25.1	365	2	S68679	G protein-coupled
5	415	23.5	373	2	A47556	ATP receptor P2u -
6	414.5	23.4	420	2	I51667	thrombin receptor
7	390.5	22.1	375	2	A54946	P-2U nucleotide re
8	389.5	22.0	328	2	I55450	G protein-coupled
9	382	21.6	432	2	A43448	thrombin receptor
10	379	21.4	361	2	B45680	G protein-coupled
11	374.5	21.2	328	2	JC4800	P2Y6

RESULT 1

JC4737

G protein-coupled receptor P2Y1 - human
 N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
 C;Species: Homo sapiens (man)
 C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000
 C;Accession: JC4737; JC4615; S54253
 R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
 A;Title: Cloning and tissue distribution of the human P2Y1 receptor.
 A;Reference number: JC4737; MUID:96205320; PMID:8630005
 A;Accession: JC4737
 A;Molecule type: DNA
 A;Residues: 1-373 <JAN>
 A;Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g1839439
 R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
 A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
 A;Reference number: JC4615; MUID:96158962; PMID:8579591
 A;Accession: JC4615
 A;Molecule type: mRNA
 A;Residues: 1-373 <AYY>
 A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731

A;Experimental source: erythro leukemia cells
 R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
 submitted to the EMBL Data Library, May 1995
 A;Description: Cloning of a human putative P2Y receptor.
 A;Reference number: S54253
 A;Accession: S54253
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-137,139-373 <LEO>
 A;Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836
 C;Comment: This receptor belongs to a family of G protein-coupled receptors. It responds to both ADP and ATP, and has several serine/threonine phosphorylation residues in the carboxyl terminus.
 C;Genetics:
 A;Gene: p2Y1; GDB:P2RY1
 A;Cross-references: GDB:677125; OMIM:601167
 A;Map position: 3pter-3qter
 C;Superfamily: ATP receptor P2u
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;52-77/Domain: transmembrane #status predicted <TM1>
 F;88-111/Domain: transmembrane #status predicted <TM2>
 F;124-152/Domain: transmembrane #status predicted <TM3>
 F;171-191/Domain: transmembrane #status predicted <TM4>
 F;214-237/Domain: transmembrane #status predicted <TM5>
 F;261-282/Domain: transmembrane #status predicted <TM6>
 F;305-328/Domain: transmembrane #status predicted <TM7>
 F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
 F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-dependent kinase) #status predicted

Query Match 29.7%; Score 525.5; DB 2; Length 373;
 Best Local Similarity 34.5%; Pred. No. 1e-37;
 Matches 106; Conservative 64; Mismatches 118; Indels 19; Gaps 3;

 Qy 24 CTDENIPLKMHYLPVIIYGIIFLVGFPGNNAVISTYIFKMRPWKSSTIIMLNLA
 Db 42 CALTKTGFQFYYPAVVILVFIIGFLGNSVAIWFMVFHMKPWSGISVYMFNLALADFLYV

 Qy 84 TSLPFLIHYIASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIHPMSCFS 143
 Db 102 LTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLGYGSILFLTCISAHRYSGVVYPLKSLG 161

 Qy 144 IHKTRCAVVAACAVVVIISLVAVIPMTFLITSTNRTNRS-ACLDLTSSDELNTIKWYNLIL 202
 Db 162 RLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTTICDTSDEYLRSYIFIYSMCT 221

 Qy 203 TASTFCLPLVIVTLCYTTIHTLTHGLQTDCLKQKARRLTILLLA
 Db 222 TVAMFCVPLVLILGYGLIVRALIYKLDNSPLRRKSIYLVIVLTVFAVSYIPFHVMKT 281

 Qy 263 IQDRISACFQSVPPLRIRSMKLTSLDH-----YAALNTFGNLLLYVVVSDNFQQ 312
 Db 282 MNLRARLDFQTPA-----MCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR 333

 Qy 313 AVCSTVR 319
 Db 334 RLSRATR 340

RESULT 2

S33733

G protein-coupled receptor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999

C;Accession: S33733
R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.;
Burnstock, G.; Barnard, E.A.
FEBS Lett. 324, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A;Reference number: S33733; MUID:93285340; PMID:8508924
A;Accession: S33733
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Cross-references: EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395085
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match          29.7%; Score 525; DB 2; Length 362;
Best Local Similarity 33.5%; Pred. No. 1.e-37;
Matches 113; Conservative 62; Mismatches 136; Indels 26; Gaps 5;

Qy      1 MNEPLDYLANASDFPDYAA---AFGN---CTDENIPLKMHYLPIYGIIFLVGFPGN 53
       | | | | | : | | | | | : : : || | : : | | | : |
Db      1 MTEALISAALNGTQPPELLAGGWAAAGNATTKCSDLTKGQFYYLPTVYILVFITGFLGS 60

Qy      54 VISTYIFKMRPWKSSTIIMLNIACTDLYLTSLPFLIHYYASGENWIFGDFMCKFIRFS 113
       | : | | | | : | | | | | : | | | | | : | | | | | |
Db      61 AIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYFNKTDWIFGDVMCKLQRF 120

Qy      114 HFNLYSSILFLTCFSIFRYCVIIHPMSCFSIHTRCAVVACAVVWIISLVAVIPMTFLI- 172
       | | | | | | | : | | : | : | | : | | : | : | : | :
Db      121 HVNLGYGSILFLTCISVHRYTGVVHPLKSLGRLKKNAVYVSSLWALVVAVIAPILFYSG 180

Qy      173 TSTNRNRSACDLTSSDELNTIKWYNLILTASTFCPLPLVIVTLCYTTIHTLTHGLQTD 232
       | | | | | | : | : | : | : | | | | | : | | : | : | :
Db      181 TGVRNKTITCYDTTADEYLRSYFVYSMCTTVFMPFCIPFIVILGCYGLIVKALIYKDLDN 240

Qy      233 SCLKQKARRLTLLLAFYVCFLPFHILRVIQDRISACFQSVPVLRIRSMKLTSDLH-- 290
       | | :: | | | : | | : | | : | | : | | | : | | : | | :
Db      241 SPLRRKSIYLVIIIVLTVFAVSYLPFHVMKTLNRLRARLDFQ-----TPQMCNFNDK 292

Qy      291 -----YAALNTFGNLLLYVVVSNDNFQQAVCSTVR 319
       | | :: | | : | | : | | : | | :
Db      293 ATYQVTRGLASLNCSVDPILYFLAGDTFRRLRSRATR 329

```

RESULT 3

JC4162

P2Y receptor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999

C;Accession: JC4162

R; Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.

Biochem. Biophys. Res. Commun. 212, 648-656, 1995

A;Title: Cloning and characterisation of a bovine P2Y receptor.

A;Reference number: JC4162; MUID:95352058; PMID:7626079

A;Accession: JC4162

A; Molecule type: mRNA

A;Residues: 1-373 <HEN>

A;Cross-references: EMBL:X87628; NID:q1032484; PIDN:CAA60958.1; PID:q1032485

A: Experimental source: aortic endothelial cell

II. EXPERIMENTAL

A:Gene: bovp2w

C:Superfamily: ATP receptor P2U

C:Keywords: glycoprotein; phosphoprotein; receptor; ti-

E: 53-77/Domain: transmembrane #status predicted <TM1>

F;52-77/Domain: transmembrane #status predicted <TM1>
E;88-111/Domain: transmembrane #status predicted <TM2>

F;88-111/Domain: transmembrane #status predicted <TM2>
E;124_150/Domain: transmembrane #status predicted <TM3>

F;124-150/Domain: transmembrane #status predicted <TM3>
E;171-181/Domain: transmembrane #status predicted -<TM4>

F;171-191/Domain: transmembrane #status predicted <TM4>
E;214-223/Domain: transmembrane #status predicted TM4

F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 29.6%; Score 523.5; DB 2; Length 373;
Best Local Similarity 34.5%; Pred. No. 1.5e-37;
Matches 106; Conservative 64; Mismatches 118; Indels 19; Gaps 3;

Qy 24 CTDENIPLKMHYLPVIYGIIFLVGFPGNNAVVISTYIFKMRPWKSSTIIMLNLA
CTDENIPLKMHYLPVIYGIIFLVGFPGNNAVVISTYIFKMRPWKSSTIIMLNLA
Db 42 CALTKTGFQFYYPAVVYLVFIIGFLGNSVAIW
CALTKTGFQFYYPAVVYLVFIIGFLGNSVAIW
Qy 84 TSLPFLIHYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIHP
MSCSFS 143
TSLPFLIHYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIHP
Db 102 LTLPALIFYYFNKTDWIFGDAMCKLQRIFHVNLYGSILFLTCISAH
RYSGVVYPLKSLG 161
LTLPALIFYYFNKTDWIFGDAMCKLQRIFHVNLYGSILFLTCISAH
Qy 144 IHKTRCAVVACAVVVIISLVA
VAPIPMFLITSTNRTNR
S-ACLDLTSSDELNTIKWYNLIL 202
IHKTRCAVVACAVVVIISLVA
VAPIPMFLITSTNRTNR
Db 162 RLKKKNAVYISV
LVLIVVVGISP
ILFYSGTGIRKNKTITCYD
TTSDEYLRSYFIYSMCT 221
RLKKKNAVYISV
LVLIVVVGISP
ILFYSGTGIRKNKTITCYD
TTSDEYLRSYFIYSMCT
Qy 203 TASTFCLPLV
IIVTLCYTTI
IHTLTHGLQ
TDSCLKQKARR
LTILLAFYVC
FLPFHILRV 262
TASTFCLPLV
IIVTLCYTTI
IHTLTHGLQ
TDSCLKQKARR
Db 222 TVAMFCVPLV
LILGCYGLIV
RALIYKDLD
NSPLRRKSIY
LVIIVLTVFA
SYIPFHVMKT 281
TVAMFCVPLV
LILGCYGLIV
RALIYKDLD
NSPLRRKSIY
Qy 263 IQDRISACFQS
VVPLRIRSM
KLT
SFLDH-----
YAALNTFGN
LLLYVV
SDNFQQ 312
IQDRISACFQS
VVPLRIRSM
KLT
SFLDH-----
YAALNTFGN
LLLYVV
SDNFQQ
Db 282 MNLRARL
DFQ-----
TPEMC
AFNDRV
YATYQV
TRGLAS
LNSCVD
PILYFLAG
DTFRR 333
MNLRARL
DFQ-----
TPEMC
AFNDRV
YATYQV
TRGLAS
LNSCVD
PILYFLAG
DTFRR
Qy 313 AVCSTVR 319
: |
Db 334 RLSRATR 340

RESULT 5

A47556

ATP receptor P2u - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999

C;Accession: A47556

R;Lustig, K.D.; Shiao, A.K.; Brake, A.J.; Julius, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993

A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.

A;Reference number: A47556; MUID:93281707; PMID:7685114

A;Accession: A47556

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-373 <LUS>

A;Cross-references: GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458

C;Superfamily: ATP receptor P2u

C;Keywords: transmembrane protein

Query Match 23.5%; Score 415; DB 2; Length 373;
Best Local Similarity 33.7%; Pred. No. 3.2e-28;
Matches 82; Conservative 50; Mismatches 101; Indels 10; Gaps 2;

Qy 28 NIPLKM
HYLPVIYGI
IFLVG
FPGNNAVV
ISTYIFK
MRPWKS
STIIMLN
LA
CTD
LLY
LTS
LP 87
NIPLKM
HYLPVIYGI
IFLVG
FPGNNAVV
ISTYIFK
MRPWKS
STIIMLN
LA
CTD
LLY
LTS
LP
Db 28 NEDFKYV
LVPVS
YGV
CVL
GLCL
NV
VALY
IF
L
C
R
L
K
T
W
N
A
T
Y
M
F
H
L
A
V
S
D
S
L
Y
A
A
S
L
P 87
NEDFKYV
LVPVS
YGV
CVL
GLCL
NV
VALY
IF
L
C
R
L
K
T
W
N
A
T
Y
M
F
H
L
A
V
S
D
S
L
Y
A
A
S
L
P
Qy 88 FLIHY
YASGENW
IFGDF
MCKFIR
FSFH
FNLYSS
ILFL
TCFS
IFRY
CVII
HP
MSCS
SIHK
T 147
FLIHY
YASGENW
IFGDF
MCKFIR
FSFH
FNLYSS
ILFL
TCFS
IFRY
CVII
HP
MSCS
SIHK
T
Db 88 LLV
YYYARG
DHWP
FSTV
LCKL
VRFL
FYTN
LYCS
ILFL
TCIS
VR
CLG
V
RPL
H
SLRG
RA 147
LLV
YYYARG
DHWP
FSTV
LCKL
VRFL
FYTN
LYCS
ILFL
TCIS
VR
CLG
V
RPL
H
SLRG
RA
Qy 148 RC
AVV
ACAVV
VI
ISL
VA
VAPI
PMFL
ITST
NRT
NR
SA
C
L
D
L
T
S
S
D
E
L
N
T
I
K
W
Y
N
L
I
L
T
A
S
T
F 207
RC
AVV
ACAVV
VI
ISL
VA
VAPI
PMFL
ITST
NRT
NR
SA
C
L
D
L
T
S
S
D
E
L
N
T
I
K
W
Y
N
L
I
L
T
A
S
T
F
Db 148 RYARR
VA
AVV
W
VL
AC
QAP
VLY
FV
TTS
VR
GTR
ITCH
DTS
ARE
L
F
SH
F
V
AY
SS
V
ML
G
L
F 207
RYARR
VA
AVV
W
VL
AC
QAP
VLY
FV
TTS
VR
GTR
ITCH
DTS
ARE
L
F
SH
F
V
AY
SS
V
ML
G
L
F
Qy 208 CL
PLV
IIV
TLC
YTT
I
H
T
L

TH
G
L
Q
T
D
S
C
L
K
Q
K
A
R
R
L
T
I
L
L
L
A
F
Y
V
C
F
L
P
H
I
L
260
CL
PLV
IIV
TLC
YTT
I
H
T
L

TH
G
L
Q
T
D
S
C
L
K
Q
K
A
R
R
L
T
I
L
L
L
A
F
Y
V
C
F
L
P
H
I
L
Db 208 AV
PFS
V
I
L
C
Y
V
L
M
A
R
R
L
K
P
A
Y
G
T
G
G
L
P
R

A
K
R
K
S
V
R
T
I
A
L
V
L
A
F
C
L
P
F
H
V
T
264
AV
PFS
V
I
L
C
Y
V
L
M
A
R
R
L
K
P
A
Y
G
T
G
G
L
P
R

A
K
R
K
S
V
R
T
I
A
L
V
L
A
F
C
L
P
F
H
V
T

Qy 261 RVI 263
| :
Db 265 RTL 267